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<!--StartFragment-->RESULT 1
SART3_HUMAN
ID   SART3_HUMAN                Reviewed;          963 AA.
AC   Q15020; Q2M2H0; Q58F06; Q8IU51; Q96J95;
DT   07-FEB-2006, integrated into UniProtKB/Swiss-Prot.
DT   01-NOV-1996, sequence version 1.
DT   21-AUG-2007, entry version 57.
DE   Squamous cell carcinoma antigen recognized by T-cells 3 (SART-3)
DE   (hSART-3) (Tat-interacting protein of 110 kDa) (Tip110).
GN   Name=SART3; Synonyms=KIAA0156, TIP110;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND SUBCELLULAR LOCATION.
RX   PubMed=10463607;
RA   Yang D., Nakao M., Shichijo S., Sasatomi T., Takasu H., Matsumoto H.,
RA   Mori K., Hayashi A., Yamana H., Shirouzu K., Itoh K.;
RT   "Identification of a gene coding for a protein possessing shared tumor
RT   epitopes capable of inducing HLA-A24-restricted cytotoxic T
RT   lymphocytes in cancer patients.";
RL   Cancer Res. 59:4056-4063(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2), TISSUE SPECIFICITY,
RP   SUBCELLULAR LOCATION, FUNCTION, AND INTERACTION WITH TAT.
RC   TISSUE=Fetal brain;
RX   MEDLINE=22075130; PubMed=11959860; DOI=10.1074/jbc.M200773200;
RA   Liu Y., Li J., Kim B.O., Pace B.S., He J.J.;
RT   "HIV-1 Tat protein-mediated transactivation of the HIV-1 long terminal
RT   repeat promoter is potentiated by a novel nuclear Tat-interacting
RT   protein of 110 kDa, Tip110.";
RL   J. Biol. Chem. 277:23854-23863(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   TISSUE=Bone marrow;
RX   MEDLINE=96127530; PubMed=8590280; DOI=10.1093/dnares/2.4.167;
RA   Nagase T., Seki N., Tanaka A., Ishikawa K., Nomura N.;
RT   "Prediction of the coding sequences of unidentified human genes. IV.
RT   The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by
RT   analysis of cDNA clones from human cell line KG-1.";
RL   DNA Res. 2:167-174(1995).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORMS 1 AND 3).
RC   TISSUE=Brain, Eye, Skin, and Uterus;
RX   PubMed=15489334; DOI=10.1101/gr.2596504;
RG   The MGC Project Team;
RT   "The status, quality, and expansion of the NIH full-length cDNA
RT   project: the Mammalian Gene Collection (MGC).";
RL   Genome Res. 14:2121-2127(2004).
RN   [5]
RP   PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT SER-10 AND SER-16, AND MASS
RP   SPECTROMETRY.
RC   TISSUE=Epithelium;
RX   PubMed=17081983; DOI=10.1016/j.cell.2006.09.026;
RA   Olsen J.V., Blagoev B., Gnäd F., Macek B., Kumar C., Mortensen P.,
RA   Mann M.;
RT   "Global, in vivo, and site-specific phosphorylation dynamics in
RT   signaling networks.";
RL   Cell 127:635-648(2006).

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RN      [6]
RP      PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT SER-852, AND MASS
RP      SPECTROMETRY.
RX      PubMed=17525332; DOI=10.1126/science.1140321;
RA      Matsuoka S., Ballif B.A., Smogorzewska A., McDonald E.R. III,
RA      Hurov K.E., Luo J., Bakalarski C.E., Zhao Z., Solimini N.,
RA      Lerenthal Y., Shiloh Y., Gygi S.P., Elledge S.J.;
RT      "ATM and ATR substrate analysis reveals extensive protein networks
RT      responsive to DNA damage.";
RL      Science 316:1160-1166(2007).
CC      -!- FUNCTION: Regulates Tat transactivation activity through direct
CC      interaction. May be a cellular factor for HIV-1 gene expression
CC      and viral replication.
CC      -!- SUBUNIT: Interacts with HIV-1 Tat.
CC      -!- SUBCELLULAR LOCATION: Cytoplasm. Nucleus speckle. Note=Localized
CC      in speckles. Expressed in the nucleus of all of the malignant
CC      tumor cell lines tested and the majority of cancer tissues with
CC      various histologies, including squamous cell carcinomas (SCC),
CC      adenocarcinomas, melanomas and leukemias cells. However, this
CC      protein is undetectable in the nucleus of any cell lines of
CC      nonmalignant cells or normal tissues, except for the testis.
CC      Expressed in the cytoplasm of all the proliferating cells,
CC      including normal and malignant cells, but not in normal tissues,
CC      except for the testis and the fetal liver.
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=3;
CC      Name=1;
CC      IsoId=Q15020-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q15020-2; Sequence=VSP_017250, VSP_017251;
CC      Note=No experimental confirmation available;
CC      Name=3;
CC      IsoId=Q15020-3; Sequence=VSP_017248, VSP_017249;
CC      Note=No experimental confirmation available;
CC      -!- TISSUE SPECIFICITY: Ubiquitously expressed.
CC      -!- PTM: Phosphorylated upon DNA damage, probably by ATM or ATR.
CC      -!- SIMILARITY: Contains 8 HAT repeats.
CC      -!- SIMILARITY: Contains 2 RRM (RNA recognition motif) domains.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AF387506; AAK69347.1; -; mRNA.
DR      EMBL; AB020880; BAA78384.1; -; mRNA.
DR      EMBL; D63879; BAA09929.1; -; mRNA.
DR      EMBL; BC032601; AAH32601.1; -; mRNA.
DR      EMBL; BC041638; AAH41638.1; -; mRNA.
DR      EMBL; BC093784; AAH93784.1; -; mRNA.
DR      EMBL; BC103706; AAI03707.1; -; mRNA.
DR      EMBL; BC111983; AAI11984.1; -; mRNA.
DR      UniGene; Hs.584842; -.
DR      HSSP; Q14103; 1IQT.
DR      IntAct; Q15020; -.
DR      PeptideAtlas; Q15020; -.
DR      Ensembl; ENSG00000075856; Homo sapiens.
DR      HGNC; HGNC:16860; SART3.
DR      PharmGKB; PA34948; -.
DR      ArrayExpress; Q15020; -.
DR      GermOnline; ENSG00000075856; Homo sapiens.
DR      InterPro; IPR012677; a_b_plait_nuc_bd.
DR      InterPro; IPR003107; HAT.

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DR InterPro; IPR008669; Lsm_interact.
 DR InterPro; IPR000504; RRM_RNP1.
 DR Gene3D; G3DSA:3.30.70.330; a_b_plait_nuc_bd; 2.
 DR Pfam; PF05391; Lsm_interact; 1.
 DR Pfam; PF00076; RRM_1; 2.
 DR SMART; SM00386; HAT; 7.
 DR SMART; SM00360; RRM; 2.
 DR PROSITE; PS0102; RRM; 2.
 PE 1: Evidence at protein level;
 KW Alternative splicing; Coiled coil; Cytoplasm; Nucleus;
 KW Phosphorylation; Repeat; RNA-binding.
 FT CHAIN 1 963 Squamous cell carcinoma antigen
 FT recognized by T-cells 3.
 FT /FTid=PRO_0000223313.
 FT REPEAT 126 158 HAT 1.
 FT REPEAT 164 195 HAT 2.
 FT REPEAT 201 237 HAT 3.
 FT REPEAT 242 275 HAT 4.
 FT REPEAT 324 356 HAT 5.
 FT REPEAT 359 391 HAT 6.
 FT REPEAT 394 430 HAT 7.
 FT REPEAT 487 520 HAT 8.
 FT DOMAIN 704 782 RRM 1.
 FT DOMAIN 801 878 RRM 2.
 FT REGION 600 670 Required for nuclear localization.
 FT COILED 21 46 Potential.
 FT COILED 82 110 Potential.
 FT COILED 559 619 Potential.
 FT MOTIF 601 617 Nuclear localization signal (Potential).
 FT COMBIAS 89 92 Poly-Glu.
 FT COMBIAS 612 616 Poly-Lys.
 FT MOD_RES 10 10 Phosphoserine.
 FT MOD_RES 16 16 Phosphoserine.
 FT MOD_RES 852 852 Phosphoserine.
 FT VAR_SEQ 105 129 LSINVDYNCHVDLIRLLRLEGELT -> VGPVGSGHLPV
 FT FQVLGSPCPGPPP (in isoform 3).
 FT /FTid=VSP_017248.
 FT VAR_SEQ 130 963 Missing (in isoform 3).
 FT /FTid=VSP_017249.
 FT VAR_SEQ 351 364 SQYLDRLQKVKDLV -> RSTTESKGFGFICT (in
 FT isoform 2).
 FT /FTid=VSP_017250.
 FT VAR_SEQ 365 963 Missing (in isoform 2).
 FT /FTid=VSP_017251.
 SQ SEQUENCE 963 AA; 109935 MW; 06B26CEB8B19102A CRC64;

 Query Match 100.0%; Score 963; DB 1; Length 963;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 963; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MATAAETSASEPEAEKAGPKADGEEDEVKAARTRRKVLSRAVAAATYKTMGPAWDQQEE 60
 Db 1 MATAAETSASEPEAEKAGPKADGEEDEVKAARTRRKVLSRAVAAATYKTMGPAWDQQEE 60

 QY 61 GVSES DGDEYAMASSAESSPGYEWEYDEEEKNQLEIERLEEQLSINVDYNCHVDLIR 120
 Db 61 GVSES DGDEYAMASSAESSPGYEWEYDEEEKNQLEIERLEEQLSINVDYNCHVDLIR 120

 QY 121 LLRLEGELTKVRMARQKMFIFPLTEELWLEWLHDEISMAQDGLDREHYVDLFEKAVKDY 180
 Db 121 LLRLEGELTKVRMARQKMFIFPLTEELWLEWLHDEISMAQDGLDREHYVDLFEKAVKDY 180

Qy	181	ICPNIWLEYGQYSVGGIGQGKGGLEKVRSVFERALSSVGLHMTKGLALWEAYREFESAIVE	240
Db	181	ICPNIWLEYGQYSVGGIGQGKGGLEKVRSVFERALSSVGLHMTKGLALWEAYREFESAIVE	240
Qy	241	AARLEKVHSLFRRLQLAIPLYDMEATFAEYEEWSEDPIPESVIQNYNKALQQLEKYKPYEE	300
Db	241	AARLEKVHSLFRRLQLAIPLYDMEATFAEYEEWSEDPIPESVIQNYNKALQQLEKYKPYEE	300
Qy	301	ALLQAEAPRLAEYQAYIDFEMKIGDPARIQLIFERALVENCVLDPDLWIRYSQYLDRLQKV	360
Db	301	ALLQAEAPRLAEYQAYIDFEMKIGDPARIQLIFERALVENCVLDPDLWIRYSQYLDRLQKV	360
Qy	361	KDLVLSVHNRAIRNCPWTVALWSRYLLAMERHGVHDQVISVTFEKNALNAGFIQATDYVEI	420
Db	361	KDLVLSVHNRAIRNCPWTVALWSRYLLAMERHGVHDQVISVTFEKNALNAGFIQATDYVEI	420
Qy	421	WQAYLDYLRRRVDFKQDSSKEELELRAAFTRALEYLKQVEVERFNESEGDPSVIMQNWAR	480
Db	421	WQAYLDYLRRRVDFKQDSSKEELELRAAFTRALEYLKQVEVERFNESEGDPSVIMQNWAR	480
Qy	481	IEARLCNNMQKARELWDSIMTRGNAKYANMWLEYYNLERAHGDTQHCRKALHRAVQCTSD	540
Db	481	IEARLCNNMQKARELWDSIMTRGNAKYANMWLEYYNLERAHGDTQHCRKALHRAVQCTSD	540
Qy	541	YPEHVCEVLLTMRTEGSLEDWDIAVQKTETRLARVNEQRMKAAEKEAALVQQEEKAEQ	600
Db	541	YPEHVCEVLLTMRTEGSLEDWDIAVQKTETRLARVNEQRMKAAEKEAALVQQEEKAEQ	600
Qy	601	RKRARAEEKKALKKKKIRGPEKRGADEDDEKEWGDDEEQQSKRRRVENSIPAAGETQNV	660
Db	601	RKRARAEEKKALKKKKIRGPEKRGADEDDEKEWGDDEEQQSKRRRVENSIPAAGETQNV	660
Qy	661	EVAAGPAGKCAAVDVEPPSKQKEKAASLKRDMPKVLHSDSKDSITVFSNLPYSMQEPDT	720
Db	661	EVAAGPAGKCAAVDVEPPSKQKEKAASLKRDMPKVLHSDSKDSITVFSNLPYSMQEPDT	720
Qy	721	KLRPLFEACGEVVQIRPIFSNRGDFRGYCYVEFKEEKSALQALEMDRKSVEGRPMFVSPC	780
Db	721	KLRPLFEACGEVVQIRPIFSNRGDFRGYCYVEFKEEKSALQALEMDRKSVEGRPMFVSPC	780
Qy	781	VDKSKNPDFKVFRYSTSLEKHKLFISGLPFSCTEELEEICKAHGTVKDLRLVTNRAGKP	840
Db	781	VDKSKNPDFKVFRYSTSLEKHKLFISGLPFSCTEELEEICKAHGTVKDLRLVTNRAGKP	840
Qy	841	KGLAYVEYENESQASQAVMKMDGMTIKENIIKVAISNPPQRKVPEKPETRKAPGGPMLLP	900
Db	841	KGLAYVEYENESQASQAVMKMDGMTIKENIIKVAISNPPQRKVPEKPETRKAPGGPMLLP	900
Qy	901	QTYGARGKGRQTLSELLPRALQRPSSAAPQAENGPAAPAVAAPATEAPKMSNADFAKLF	960
Db	901	QTYGARGKGRQTLSELLPRALQRPSSAAPQAENGPAAPAVAAPATEAPKMSNADFAKLF	960
Qy	961	LRK 963	
Db	961	LRK 963	

<!--EndFragment-->